

DW Pur/09

Serial Number: 09/830,123

CRF Processing Date: 11/3/2002

Edited by: AC

Verified by: AC

(STIC stat

ENTERED

#7

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings-used by an applicant, specifically:
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seqs 2, 17 - aligned amino acid nos.

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,123

DATE: 01/03/2002

TIME: 22:55:21

Input Set : A:\PTO.txt

Output Set: N:\CRF3\01032002\I830123.raw

4 <110> APPLICANT: Iida, Shigeru
5 Tanaka, Sachiko
6 Inagaki, Yoshishige
8 <120> TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
10 <130> FILE REFERENCE: 001560-397
12 <140> CURRENT APPLICATION NUMBER: 09/830,123
13 <141> CURRENT FILING DATE: 2001-04-24
15 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05722
16 <151> PRIOR FILING DATE: 2000-08-24
18 <150> PRIOR APPLICATION NUMBER: JP 11/236800
19 <151> PRIOR FILING DATE: 1999-08-24
21 <160> NUMBER OF SEQ ID NOS: 20
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2237
27 <212> TYPE: DNA
28 <213> ORGANISM: Ipomoea nil
30 <220> FEATURE:
31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: (1)..(2237)
33 <223> OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating
the
34 pH of vacuoles
36 <400> SEQUENCE: 1
37 agaatgtagg ctacagaaat tttcagacag atagatacat aaatccgtat aatagagaca 60
39 gagaaacaga aaaagagaga gtcacgttaa tcctgagatt ttcctccatt tgtctgaagc 120
41 tcttcatacct tcaacactac cccacatct cacccttcaa gtgatttgta tgttttcggg 180
43 agggattgga atgggcaacc cggatatgtg aacagaaacc acgacattgg gaaaagattt 240
45 attgcaaaaa ttgttttgat tgttttgat tttgtggtag aaaaagggga agaacaaaa 299
47 atg gcg ttc ggg ttg tct tct ttg ctc caa aat tcg gat ttg ttc acg 347
48 Met Ala Phe Gly Leu Ser Ser Leu Leu Gln Asn Ser Asp Leu Phe Thr
49 1 5 10 15
51 tct gat cat gct tcc gtt gtg tcg atg aac ctc ttt gtg gcg ttg ctt 395
52 Ser Asp His Ala Ser Val Val Ser Met Asn Leu Phe Val Ala Leu Leu
53 20 25 30
55 tgc gca tgc att gtt ctt ggc cat cta ctc gag gag aat cgc tgg gtg 443
56 Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val
57 35 40 45
59 aac gaa tcc att act gcc ctt ata att ggt ttg tgc acc gga gtt gta 491
60 Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
61 50 55 60
63 att ttg ctc ctt agc gga gga aag agt tca cat ctt ctc gtc ttt agc 539
64 Ile Leu Leu Leu Ser Gly Gly Lys Ser Ser His Leu Leu Val Phe Ser
65 65 70 75 80
67 gaa gat ctt ttc ttt ata tat ctc ctg cca cct ata ata ttc aat gcg 587
68 Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
69 85 90 95
71 ggg ttt caa gtg aaa aag aag cag ttt ttc gtg aac ttc atg aca att 635

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Input Set : A:\PTO.txt

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72 Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Val Asn Phe Met Thr Ile
73          100          105          110
75 atg ctg ttt gga gct att ggc aca ctt att agc tgt tct att ata tca      683
76 Met Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Cys Ser Ile Ile Ser
77          115          120          125
79 ttt ggt gcg gtc aaa att ttc aag cac tta gac att gac ttt ctg gat      731
80 Phe Gly Ala Val Lys Ile Phe Lys His Leu Asp Ile Asp Phe Leu Asp
81          130          135          140
83 ttt gga gat tat tta gca att ggt gcg ata ttt gct gca acc gat tct      779
84 Phe Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser
85 145          150          155          160
87 gtt tgc aca ttg cag gtg ctc agt cag gat gag acg ccc cta ctt tac      827
88 Val Cys Thr Leu Gln Val Leu Ser Gln Asp Glu Thr Pro Leu Leu Tyr
89          165          170          175
91 agt ctc gtg ttt gga gaa ggg gtc gtc aat gat gct aca tct gtg gtc      875
92 Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val
W--> 93          180          185          190
95 ctt ttt aat gct att caa agt ttt gac atg act agt ttt gat cca aaa      923
96 Leu Phe Asn Ala Ile Gln Ser Phe Asp Met Thr Ser Phe Asp Pro Lys
W--> 97          195          200          205
99 att ggg ctt cat ttc att gga aac ttc ttg tat tta ttt ctc tcg agc      971
100 Ile Gly Leu His Phe Ile Gly Asn Phe Leu Tyr Leu Phe Leu Ser Ser
W--> 101          210          215          220
103 act ttt ttg ggc gtg gga att gga ctg ctt tgt gct tat att atc aaa      1019
104 Thr Phe Leu Gly Val Gly Ile Gly Leu Leu Cys Ala Tyr Ile Ile Lys
W--> 105 225          230          235          240
107 aag cta tac ttt ggc agg cac tca acc gat cgt gag gtt gcc ctt atg      1067
108 Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met
W--> 109          245          250          255
111 atg ctc atg tct tac ttg tct tat ata atg gcc gag tta ttc tat cta      1115
112 Met Leu Met Ser Tyr Leu Ser Tyr Ile Met Ala Glu Leu Phe Tyr Leu
W--> 113          260          265          270
115 agc ggc ata ctt act gta ttc ttc tgt gga att gtc atg tct cat tat      1163
116 Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr
W--> 117          275          280          285
119 acc tgg cac aat gtt acc gag agc tca agg gtc act act agg cat tcc      1211
120 Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Arg His Ser
W--> 121          290          295          300
123 ttt gca act ctg tca ttt gtc gca gag aca ttt atc ttc ctc tat gtt      1259
124 Phe Ala Thr Leu Ser Phe Val Ala Glu Thr Phe Ile Phe Leu Tyr Val
W--> 125 305          310          315          320
127 ggt atg gat gcc ttg gat atc gag aaa tgg aaa ttt gtg aaa aat agt      1307
128 Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Lys Asn Ser
W--> 129          325          330          335
131 cag gga cta tca gtt gca gtg agc tca ata ttg gta ggc cta atc tta      1355
132 Gln Gly Leu Ser Val Ala Val Ser Ser Ile Leu Val Gly Leu Ile Leu
W--> 133          340          345          350
135 gta ggc aga gct gcg ttc gta ttc ccc ttg tcg ttt tta tcc aac tta      1403
136 Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu

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W--> 137          355          360          365
      139 gca aag aaa aac tct tcg gac aag ata tcc ttt agg caa caa ata ata 1451
      140 Ala Lys Lys Asn Ser Ser Asp Lys Ile Ser Phe Arg Gln Gln Ile Ile
W--> 141          370          375          380
      143 att tgg tgg gct ggc cta atg aga ggc gcc gtc tca ata gca ctt gcg 1499
      144 Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
W--> 145 385          390          395          400
      147 tat aat aag ttt aca acc tcg ggg cat acg tca ttg cac gag aac gca 1547
      148 Tyr Asn Lys Phe Thr Thr Ser Gly His Thr Ser Leu His Glu Asn Ala
W--> 149          405          410          415
      151 ata atg att aca agt act gtt acg gtt gtt ctg ttc agc aca gtt gta 1595
      152 Ile Met Ile Thr Ser Thr Val Thr Val Val Leu Phe Ser Thr Val Val
W--> 153          420          425          430
      155 ttc ggg ttg atg acg aag cct ctg ata aac ctt ctg cta ccc ccg cac 1643
      156 Phe Gly Leu Met Thr Lys Pro Leu Ile Asn Leu Leu Leu Pro Pro His
W--> 157          435          440          445
      159 aag cag atg cca agc ggt cat tcg tca atg aca aca tcc gaa ccc agt 1691
      160 Lys Gln Met Pro Ser Gly His Ser Ser Met Thr Thr Ser Glu Pro Ser
W--> 161          450          455          460
      163 agt ccg aag cac ttc acg gtg cca ctc ctg gac aac caa cct gac tca 1739
      164 Ser Pro Lys His Phe Thr Val Pro Leu Leu Asp Asn Gln Pro Asp Ser
W--> 165 465          470          475          480
      167 gaa agc gat atg ata acc gga cct gag gtt gct cga cca act gcc ttg 1787
      168 Glu Ser Asp Met Ile Thr Gly Pro Glu Val Ala Arg Pro Thr Ala Leu
W--> 169          485          490          495
      171 cgc atg ctg cta agg acg cca acc cac acc gtg cac cgc tac tgg cgt 1835
      172 Arg Met Leu Leu Arg Thr Pro Thr His Thr Val His Arg Tyr Trp Arg
W--> 173          500          505          510
      175 aag ttt gat gat tcg ttt atg cgt ccc gtg ttt ggc ggg cgg gga ttc 1883
      176 Lys Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe
W--> 177          515          520          525
      179 gtt ccg ttt gtc gcg ggc tca cca gtt gag cag agc cct aga tga 1928
      180 Val Pro Phe Val Ala Gly Ser Pro Val Glu Gln Ser Pro Arg
W--> 181          530          535          540
      183 ggtacaaagt acaaacaaga cactgttgct ggggtgaaata gtgtaagttg tatcatagtt 1988
      185 gattctggtt gccctcttta tgaaatgggc tgggtgaaag tcttctcact agctagggtg 2048
      187 cattgcattg ctacttcata aatgttttat tttattttgt aaatgttggt gcattttagg 2108
      189 tacttgattt aacacctcat ttgtagcata ttatttggtg cagagtattt tttttatgaa 2168
      191 acaataatgg ctgaattatc aatttggctc tatgttttga tgcttagtaa aaaaaaaaaa 2228
      193 aaaaaaaaaa 2237
      196 <210> SEQ ID NO: 2
      197 <211> LENGTH: 542
      198 <212> TYPE: PRT
      199 <213> ORGANISM: Ipomea nil
      201 <220> FEATURE:
      202 <221> NAME/KEY: peptide
      203 <222> LOCATION: (1)..(542)
      204 <223> OTHER INFORMATION: Amino acid sequence of protein regulating the pH of vacuoles
      207 <400> SEQUENCE: 2

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RAW SEQUENCE LISTING

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209 Met Ala Phe Gly Leu Ser Ser Leu Leu Gln Asn Ser Asp Leu Phe Thr
210 1 5 10 15
212 Ser Asp His Ala Ser Val Val Ser Met Asn Leu Phe Val Ala Leu Leu
213 20 25 30
215 Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val
216 35 40 45
218 Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
219 50 55 60
221 Ile Leu Leu Leu Ser Gly Gly Lys Ser Ser His Leu Leu Val Phe Ser
222 65 70 75 80
224 Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
225 85 90 95
227 Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Val Asn Phe Met Thr Ile
228 100 105 110
230 Met Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Cys Ser Ile Ile Ser
231 115 120 125
233 Phe Gly Ala Val Lys Ile Phe Lys His Leu Asp Ile Asp Phe Leu Asp
234 130 135 140
236 Phe Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser
237 145 150 155 160
239 Val Cys Thr Leu Gln Val Leu Ser Gln Asp Glu Thr Pro Leu Leu Tyr
240 165 170 175
242 Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val
243 180 185 190
245 Leu Phe Asn Ala Ile Gln Ser Phe Asp Met Thr Ser Phe Asp Pro Lys
246 195 200 205
248 Ile Gly Leu His Phe Ile Gly Asn Phe Leu Tyr Leu Phe Leu Ser Ser
249 210 215 220
251 Thr Phe Leu Gly Val Gly Ile Gly Leu Leu Cys Ala Tyr Ile Ile Lys
252 225 230 235 240
254 Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met
255 245 250 255
257 Met Leu Met Ser Tyr Leu Ser Tyr Ile Met Ala Glu Leu Phe Tyr Leu
258 260 265 270
260 Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr
261 275 280 285
263 Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Arg His Ser
264 290 295 300
266 Phe Ala Thr Leu Ser Phe Val Ala Glu Thr Phe Ile Phe Leu Tyr Val
267 305 310 315 320
269 Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Lys Asn Ser
270 325 330 335
272 Gln Gly Leu Ser Val Ala Val Ser Ser Ile Leu Val Gly Leu Ile Leu
273 340 345 350
275 Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
276 355 360 365
278 Ala Lys Lys Asn Ser Ser Asp Lys Ile Ser Phe Arg Gln Gln Ile Ile
279 370 375 380
281 Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala

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Input Set : A:\PTO.txt

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282 385          390          395          400
284 Tyr Asn Lys Phe Thr Thr Ser Gly His Thr Ser Leu His Glu Asn Ala
285          405          410          415
287 Ile Met Ile Thr Ser Thr Val Thr Val Val Leu Phe Ser Thr Val Val
288          420          425          430
290 Phe Gly Leu Met Thr Lys Pro Leu Ile Asn Leu Leu Leu Pro Pro His
291          435          440          445
293 Lys Gln Met Pro Ser Gly His Ser Ser Met Thr Thr Ser Glu Pro Ser
294          450          455          460
296 Ser Pro Lys His Phe Thr Val Pro Leu Leu Asp Asn Gln Pro Asp Ser
297 465          470          475          480
299 Glu Ser Asp Met Ile Thr Gly Pro Glu Val Ala Arg Pro Thr Ala Leu
300          485          490          495
302 Arg Met Leu Leu Arg Thr Pro Thr His Thr Val His Arg Tyr Trp Arg
303          500          505          510
305 Lys Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe
306          515          520          525
308 Val Pro Phe Val Ala Gly Ser Pro Val Glu Gln Ser Pro Arg
309          530          535          540

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312 <210> SEQ ID NO: 3

313 <211> LENGTH: 16

314 <212> TYPE: DNA

315 <213> ORGANISM: Artificial Sequence

317 <220> FEATURE:

318 <223> OTHER INFORMATION: MseI adaptor

320 <400> SEQUENCE: 3

321 gacgatgagt cctgag

16

324 <210> SEQ ID NO: 4

325 <211> LENGTH: 14

326 <212> TYPE: DNA

327 <213> ORGANISM: Artificial Sequence

329 <220> FEATURE:

330 <223> OTHER INFORMATION: MseI adaptor

332 <400> SEQUENCE: 4

333 tactcaggac tcat

14

336 <210> SEQ ID NO: 5

337 <211> LENGTH: 20

338 <212> TYPE: DNA

339 <213> ORGANISM: Artificial Sequence

341 <220> FEATURE:

342 <223> OTHER INFORMATION: TIR primer

344 <400> SEQUENCE: 5

345 tgtgcatttt tcttgtagtg

20

348 <210> SEQ ID NO: 6

349 <211> LENGTH: 16

350 <212> TYPE: DNA

351 <213> ORGANISM: Artificial Sequence

353 <220> FEATURE:

354 <223> OTHER INFORMATION: MseI primer

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/830,123

DATE: 01/03/2002

TIME: 22:55:22

Input Set : A:\PTO.txt

Output Set: N:\CRF3\01032002\I830123.raw

L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:610 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:618 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:839 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:859 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:891 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:895 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:899 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:903 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:907 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:911 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:915 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

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Input Set : A:\PTO.txt

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L:923 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:1087 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:1091 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18